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Human, tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; tuston protectin, linker, TNF, IL-1; cachexia, eccebtal malaria, rheumatoid arthritis; diabetes, multiple sclenosis, septic shock; publimenary fibrosis, silicosis, ailoutaft, xemmyraft, rejection, qratt, verses host disease; sepsis; intlammation; allergy;
                         363 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 SerCysSerLysCysArglysCluMetClyClnValClulleSerSerCy 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 AGCTGCTCCAAATGCCGAAAGGAATGGGTCAAGTGCGGAAATCTCTTTG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 sThrValAspArgAspThrValCysClTCysArgLysAsnGlnTyrArgH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 CACAGTGGACCGGAACGTGTGTGTGTGTTGCAAGAAGGAGTAAGAACGAGTAACGCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 isTyrTrpSerGluAshLeuFheGlnCysFheAshCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AsnClyThrVa!HisLeuSerCysClnCluLysClnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 rCysHisAlaClyrhcPheLcuArgCluAsnCluCysValScrCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3 snCysLysLysSerLeuGlaC, sThrlysLeuCysLeuFrod1n11ed1n 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               763 ACTICTAAGAAAACOTTGGAGTGCAAGAGTTGTGGGTAAGGGGGAGATTGAG 812
                                                                                                                                                                                                                                                                                                                               40 HisProGinAsnAsnScriteCysCysThri.ysCysHisLysGlyThrTy 56
1 MetGlyLeuSerThrValProAspLeuLeuLeuReuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                        ..... AspSerValCysProGlnGlyLysTyrIle 39
                                                                                                                                                                                                                                                                                                                                                                                                                                          56 ILGUTYFASDASPCYSPFOGLYPFOGLYGINASPTHFASPCYSAFGGLUC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ49932
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ID AAQ49932 standard; cDNA to mRNA; 1368 BP.
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Homo sapiens. Lambda-gt10-7-ctnfbp,

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The linker many comparisons of 100 aminor acids acheered from 62,, Asp. Ser. Thr and Ala. These linkers separate the individual morities by such a distance that each component of the fosion protien is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachesta, rheumatoid arthritis, diabetes, multiple sclerosis, pulmonary fibrosis and silicosis, cerebral malaria, allograft and xenograft rejection in graft verses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ49931-32 encode human tuneur accrosss factor receptor (TNF-R) and the sequences in AAQ49933-34 encode human falterleakin-1 receptor (IL-IR). These sequences were used in the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                          New fusion protein tumour necrosis factor and human interleukin-l receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    host disease, sepsis, septic shock, inflammation, allergies and autoimmune dystunctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
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IL-1R-linker INF R linker-TNF-R or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclusure, Page 57·59, 85pp; English.
                 ocation/Qualifiers
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/product- hTNF-R
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                 Key
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TNPRL: tumour nectoris factor receptor, polymorphism; homan;
tumour; cancer; apoptosis; bacterial infection; ds.
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                                                                                                                              90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106
                                                                                                                                                                                   106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
                                                                                                                                                                                                                                .23 isTyrfrpSerCluAsnLeuPheClnCysPheAsnCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                           140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                    156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                               56 rLeuTyrAsaAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: //SIDSI/3/14/ara/Jenesery/processynymal/ara/AAA3/1246
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194..322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA95105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
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The present invention relates to polymorphic variants of the tumour necrosis factor receptor [ (INFR] gene. The present sequence is the coding sequence of the INFR] gene. The sequence of the whole gene is given in AAA95102, AAA95103 and AAA95104. The polymorphisms were facentified by amplitying and sequencing reasons of the gene. Twelve polymorphic had also asserted in these wells in the polymorphisms tour cause a change in the INFRI protein. The INFRI polymorphisms may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Folynauleutides comprising polynauphic satiants of a reference sequence for tumour necrosis factor receptor 1 (TMFRI), isetal for studying the biological function of TMFRI and identifying drugs targeting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for studying the biological function of INFRT as well as for identifying drugs targefug the protein for freathmunt of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related to its abnormal expression or function such as fumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis related disorders and bacterial intection.
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                               /*iag- 1
replace(269,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein for treating disorders
                   replace(224,T)
                                                                                                  replace(352.A)
                                                                                                                         1 optace (403, C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENA ) GENAISSANCE PHARM INC
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1058..1368
/*tag- p
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552..625
/*tag= 1
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740..768
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474..551
        /number-
                                                                324..472
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SCHULZ V P.
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                                                                                                                                                                                                                                                                                                                                                                     WO200050436-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEP-1999;
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                     variation
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                                          and the table
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Sequence 1888 BP; 292 A: 424 C; 225 G; 276 T; U of her;

Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;

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90 SerCysSerlysCysArglysCluMetGlyClnValGluffuSerSerCy 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 sThrValAspArgAspThrValCysGlyCysArgLysAsnClnTyrArgH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
                                                                                                                           40 HisProGlinAshAshSetileCysCysThriysCysHisLysGlyThrTy 56
                                                                                                                                                                                                                                                                                                                                      56 rLeuTyrAsnAspCysProGlyProGlyClnAspThrAspCysAigGluC 73
                                                                                                                                                                                                                                                                                                                                                                                         73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArqHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq pamer 78:1582 Apagdata Aperesang Aperesang Akala92 BarraAp20373
                                      Percent Identity, 94,787
                           Caps:
                                                                                                   Align seg 1/1 to: AAA95105 from: 1 to: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AsnVallySGlyThrGlijAspSorGlyThrThr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC20973 standard; DNA: 2062 BP
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                                                             alignment_block:
US-09.525-998A-12 x AAA95105
                        Ratio: 5.588
Percent Similarity: 94.787
          Quality: 1117.50
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aliqnment_scores:
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The sequence is that of DNA encoding tunnour necrosis factor alpha binding platental CNNA library in lambda quil using a probe (AAQLU974). The DNA also encodes the extracellular domain of human 'NN aipha receptor and as such it is useful for treating diseases where 'NN' alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically theumatoid arthritis. See also AAQ20974.
                                                                                                                                                                                                                /*tag c
/note- "encodes the extracellular domain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GOTIGHT GOT GOGAATAT ACCCCTCAGGGGTTATHGGACTGGTCCCTCAGC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Med.StytesSer Toward heads control content of 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 uLeuLeuValGlylleTyrFroSerGlyVallleGly......29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2062 BF; 429 A; 616 C; 573 C, 444 T, 0 other:
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//ote "Nomologous to probe AAQ20974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 94.787
                                                                                                                                                                                                                                        TNF alpha receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1,7 to: AAQ20973 from: 1 to: 2962
                                                                 Socation/Qualifiers
155..1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Fig 1; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                90GB-0013410.
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275..1522
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Ratio: 5 588
Percent Similarity: 94.787
                                                                                            /*tag-
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              extracellular domain.
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                                        Homo sapiens
                                                                                                                                                           misc_feature
                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                     15-JUN-1990;
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                                                                                                       sig_peptide
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us-09-525-998a-12.rng

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reysHisAlaclyPhotherouargeluAsecludysValSereysSerA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 sThrvalAspArgAspThrValCysClyCysArgiysAsaClnTyrAigH 123
40 HisProGlnAsnAsnSerlleCysCysThrLysCysHisLysClyThrTy 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 CACAGYGGACCGGGACACGTGTGYGGCGCGCAGGAAGAACAGTACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AseValLysClyThrGluAspSerClyThrThr 200
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seg_name. /SIES2/gegdata/grinseg/jenesegn/NA1992.EAL.AAg24440

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treatment; pulmenary diseases, septic shock: HIV infection; AIDS; malaria; viral meningits; graft versus host disease; autoimmune disease; rheumatoid arthritis.
                                                                                                tumour necrosis factor alpha; extragellular binding domain;
                                                                                                                                                                                                         /product- human INF-alpha
                                                                                                                                                                                                                                                                          /codon- seq:"TGG", aa:Thr
1258..1260
                                                                                                                                                                                                                                                                                                            /codon= Soq"AAG", aarlon
1433.,1435
                                                                                                                                                                          Location/Qualifiers
                                                                           Encodes TNF-alpha 55kD receptor.
          AAQ24440 standard; DNA; 2062 BP
                                                                                                                                                                                                                                                     265..1267
                                                    08-NOV-1992 (first ontry)
                                                                                                                                                                                                                                /*tag- b
/notc- "3"
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seq_documentation_block:
                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                      mat_pept.ide
                                                                                                                                                                                                                                                       mat_peptide
                                AAQ24440;
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This sequence enrodes human TNE-alpha 55kb receptor. A placenta cDNA library in 412 Ass screened with prote ANGEST4. Too hybridista clones were plaque partitled and CDNA size determined by PAGE dainst an Bos Fi directorized plage DNA. The library of two CNA courses were then sequenced. The coding region of the majority of the human TNE-alpha 55kb receptor was isolated as an EDDF transcript cloding 374 amino and closed into a mammalian cell expression were not, resulting in prTNEE. A desiration of the majority of the transmembrane day engineering a termination codon just prior to the transmembrane dormain, PCP with primers AAC2227, 8 garriagod an Bobb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restriction fragment which was closed into prinkE, giving pinERecd. DAR segmencing confined this contained the designed DAR segmence. The TNE-alpha receptor expression plasmids were then transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into monkey CLS-7 čelis.
See also AAL24444-51, AAR24090, AARL4080 84, AARL7685, AAGD9246-8
                                                                                                                                                                                                                                                                                                                                                 New polypeptide capable of binding human INF alpha - comprises first three cysteine rich subdomains of INF alpha receptor for treating autoimmune disease, septic shock, HIV etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 CYTGTH SELECTERARCCOCCAGGGGTTALLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .........AspSerValCysFroGluGlyLysTyrIle 39
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Gaps: 1
Porcost (dentity, 94.787
                                                                                                                                                                                                                                                             Brennan FM, Feldmann M, Gray PW, Turner MJC:
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             Seq. "GAC", da.ASn
                                                                                                                                                                                                                              (CHAR-) CHARING GRUSS SUNLEY RES CENT.
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                                                                                                                                                          91W5-GB31826.
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              /codon št
156...274
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Ratio: 5,588
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                                                                                     A-92020260W
                                                                                                                       30-APR-1992
                                 siq_pept.ide
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Tumbur necrosis tactor inhibitor for suppression of INF alpha and "beta useful as therapeutic agent
                                                                                                                  123 isTyrTrpSerGluAsaLeuPheGlaCysFluAsuCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                                            140 AsnGlyrhvalHisteuSerCysGlnGluLysGlnAsnThrvalCysrh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
355 CITCTACAATGACTGTCTAGGCCCGGCAGTACGGACTGCAGGGAGT 404
                                                              106 sThrValAspArqAspThrValCysGlyCysArqLysAsnGlsTyrArqH 123
                                                                                                                                                                                                                                                                                                                                                                                               173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 ACTGIAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCAGATTGAG 754
                                      7% ysGluSerGlySerPheThrAlaSerGluAsuHisLeuArqHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30kD TNF inhibitor precursor gene in lambda-gt10-7ethfbp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor; inhibitor; ss
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1D = AAQ:0883 standard: cDNA; 2088 BP
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The sequence encodes the entire 30 kD INF inhibitor. The clone from which the sequence was obtd, was isolated from a cDNA library prepd from RNA form HT947 enclls treated with PMA/PHA. The whole quene can be inserted into expression vectors for prepp. of TNF inhibitor for use in the treatment of inflammatory and degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 GTGAGAGGGGCICCTTGAGGGTTCAGAAAACGGCGCAGAGACACTGGTC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 ServysSerrys/ysArgLysGluMetGlyGlnValGlulleSerSer7y 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 is"yrTrpSerCluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 ATTATTGGAGTGAAAAGCTTTTGGAGTGCTTGAATTGGAGGCTGTGGTG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669 CTGCCATGCTATTCTAAGAGAAAACGAGAGAGTGTCTCCTGTATAGTA 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 sncystystysScrieuGlucysThrtysLeucyst.euPreGln:1eGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719 ACTIGITAAGAAAAGGCTTGGAAGTTGTGTGTTGTTGTTGTGTGATTTGAG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspSerValCysProGlnGlylysTyrile 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 HisProGlaAsaAsaSerIleCysCysThrLysCysHisLysGlyThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl
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                                                                                                                                                                           other
                                                                                                                                                                                                                                                                                                Percent Identity: 94.787
                                                                                                                                                                      Sequence 2088 BP; 439 A; 626 C, 578 G, 445 T, 0
                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAQ10883 from: 1 to: 2088
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                                                                                                                                                                                                                                                                            5.588
                                                                                                                                                                                                                                                                                                                                                                 US-09-525-998A-12 x AAQ10883
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Percent Similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present insertion relates to bumour Nectosis Factor (inF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The present sequence is the coding sequence for the presursor of 30 kba TNF inhibitor. The 30 kba TNF inhibitor can inhibit TNF alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel 30 kBa tumon mechosis factor inhibitor analog comprising a
non-mative dysteine residue cross linked with polyethylene glycol,
useful for treating inflammatory and degenerative diseases mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INF inhibitor, antiinflammatory tymour Negrosis Factor; inteliguking U.-1; inflammatory disease; degenerative disease; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 ......AspSerValCysProCluClyItysTyrile 39
Hale KK, Brewer MT, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Human 30 kDa TNF inhibitor precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uLeuLeuValGlyIleTyrProSerGlyValIleGly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Fig 21; 82pp; English.
                                                                                  seq_documentation_block:
ID AAC83946 standard; DNA; 2088 BP
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                                                                                                                                                                                                                                                                                                   02-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 rCysRisAlaClyPhePheLeuArgCluAsuCluCysValSerCysSerA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 snCystystysSoricaCluCysThrtysteaCysteaProGlaffeGlu 189
319 CACCCICAAAATAATICGATIIGGIGIACCAAGIGGGAAAAGGAAAACTA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 AGMICCICCAAAIGGGGAAAAGGAAAIGGGAAGAAGTGIIGIIG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AsudlyThrValHisLeuSerCysGluGluLysGluAshThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                619 ANTGGGACOGIGCACCICICCIGCCAGGAGAACAGAGACGGIGIGCAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 rtvalyrAsaAspôysProdyProdyGinAspihrAspôysArqStu^ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2s ysciuserclysertheibralaSerGluAsnHistAnArqHisCystAn 89
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                                                                                                                                                     40 HisProGluAsnAsnSerileCysCysThrLysCysHisLysGlyThrTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  769 AAFGTTAAGGGGACTGAGGACTCAGGAA
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ID AAQ10955 standard; cDNA; 2111
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587 ATTAITGGAGTGAAAAQTITHIQGAGTGTHIQAAHIGGAQQQTIGTGCTIC 636

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TWF-BPs (see AAPIIO72-PIIO81) and oliqonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a chwa fragment for use as aprobe to serven a human placental cDWA bank constructed in lambda gill. Positive clones were identified and sequenced. DNA constructs comprising the TWF-BP coding sequence may also contain a fragment encoding a human Iq domain Recombinant constructs are used to transform relis to confer
                                                                                                                                                                                                                                                                                                                                                           Partial amino acid sequences were determined for the 55 and 75kD
                                                                                                                                                                                                    Inscluble tumour necrosis factor binding proteins \cdot and \mathsf{DNA} enceding them, useful in pharmaceutical prods, and for antibody
                                                     Lotscher H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 CACCCTCAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.37 GTGAGGGGGGGTTGAGGGCTTGAGAAAAGGAGGTGAGAGTGCCTC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 SerCysSerLysCysArqLysGluMe!GlyGlmValGluIleSerSerCy 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 HisProGloAsnAsnSerll=CysCysThrLysCysHicLysGlyThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ysGluScrGlySerFheFhrAlaSerGraAsnHisheuArgHisCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2111 RP; 445 A; 628 C; 588 G; 450 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 94.787
                                                     Dembir Z, Gent. R, Lesslauer W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 ut.eut.euValGlylleTyrProSerGlyValileGly.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAQ10955 from: 1 to: 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             improved TNF-binding properties.
                                                                                                                                                                                                                                                                                                         Claim 4; Fig 1; 26pp; German.
(HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-525-998A-12 x AAQ10955
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                                                                                                                          WPI; 1991-081851/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AA010956.
                                                                                                                                                       7-PSDB; AAR11082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                               Brockhaus M,
Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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This invention describes novel homogeneous insoluble proteins (1), their (in)soluble tragments (1a) and their salts that can bind tunnour necrosis factor (TMF). The products of the invention have a salt inflammatory and antimalarial activity. (1) and (1a) are used (i) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory, antimalarial, treatment, septic shock, inflammation, autoimmane glomerulonephritis, cerebrai malaria, immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insoluble proteins, and fraqments, that bind to tamor necrosis factor, used to freat e.g. septic shock or cerebral malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dembig Z, Gentz P, Lesslauer W, Loetscher H;
                140 AsaGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                              156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
                                                                                                                            173 sudysLysLysSerLeuGludysThrLysLeudysLeuProGlnfleGlu 189
                                                                                                                                                                                                                                                      seq_name: /SID$2/gcgdata/geneseq/geneseqn/NA1999 ball AA709170
                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor binding protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "TNF binding protein"
                                                                                                                                                                                       190 AsnValLysGlyThreluAspSerGlyThrThr 200
                                                                                                                                                                                                                       787 AATGITAAGGGCACIGAGGACICAGGCACCACA 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
187..1554
                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAZ09170 standard; cDNA; 2111 BP.
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187..273
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274..1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                 AA209170;
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0000000x00

AAZ48479 otandard; DNA; 2161 BF

seq_documentation_block:

AAZ48475;

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glomerulonephritis, cerebral malaria, inmone responses and inflammation), (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for diagnostic determination of TNF in body fluids. Antibodies raised agains: (I) are used for attinity purification of (I). This sequence encodes a tumour necrosis factor binding protein described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELLILLI HELLI HEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 snCystystysSerteadlaCysThriysLeuCysLeuProGluileGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SThrValAspArgAspthrValCysClyCysArgLysAsnClnTyrArgH 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ysGluSerGlySerPhcThrAlaSerGluAsnHisLeuArgHisCysLeu 89
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2111 BP; 445 A; 629 C; 587 G; 450 1; 0 other;
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Ratio: 5.588
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                                                                                                                                                                                                                                                                                                             the invention.
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Seq_name. /Sous2/gradata, grasseq. grasseque NAZous. DALAND48475

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necrosis factor receptor type [ [INFR] HWA. Busic antiscusor compounds can be used in a method of inhibiting the explosion of INFR haman cells or tissues. The antiscuse compounds specifically hybridize with one or more uscletch acids escaled THTRL modulating the function of nucleic acid molecules encoding TNFR. Unlimmately modulating the amount of INFR produced. The antiscuse compounds and method are useful as research infection, including the treagents and originalises, and it is the frequency and prophylaxis of infection, including the infection of number formation. The prosents sequence
                                                                                                           Tumbour mechanic factor receptor type 1, TNFD1, antiaense; infection; triammation; tumbour formation; (NFE); anticancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostment, and presention of dispase, particularly tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides antibense compounds targeted to human tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense inhibition of tumor nectosis factor type Lexpression for
                                                                              Human tumour necrosis factor receptor (INFR) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 GCIGIIGGIGGGAAIAIACCCCICAGGGIIAIIGGACICAGGC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .. AspScrValCysProGinGlyLysTyrIle 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 ATGGGCCTCTCCACCCTCACCTGCTCCTGCCCCTGGTGCTGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example io, dormans 13-15; 54pp; English.
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                                          (first outry)
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US-09-525 998A 1_ x AA/48475
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Ratio: 5.588
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                                                                                                                                                                                                                                                                                                                                                                                                          Baker BF, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-105433/09.
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                                                                                                                                                                                                                                                                                        26-JUN-1998;
                                                                                                                                                                                                                                                                                                                               26-JUN-1998;
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                        31-MAR-2000
                                                                                                                                                                                                              US5007995-A
                                                                                                                                                                                                                                                    28-DEC 1999.
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p55, tumour necrosis tactor receptor; INF-R; human; murine; chimera; epiderma! gröwth factor receptor; MGF-R, protease, inhibitor;
                106
                                                                                                                                                                                                                                                   556 AGCIGCICCAAAIGCCGAAAGGAAATGGGTCAGGIGGAGAICTCTTCTTG 605
                                                                                                                               106 sThrValAspArgAspThrValCysClyCysArgLysAsnClnTyrArgH 123
                                                                                                                                                                   123 isTyrTrpSerGluAsnLeuPheGluCysPheAsnCysSerLeuCysLeu 139
                                                                                                                                                                            rCysHisAlaClyPhcPhcLcuArgCluAsnCluCysValSerCysSerA 173
406 CACCCTCAAAATAATTCGATTTGGTGTACCAAGTGGCCACAAAGGAAGCTA 455
                                                                        506 ÄTĞAGAGGGGTTPTTÇAPPGPTTPAGAAAAÇÇAÇTÇAGAÇAÇTGGETE 555
                                                                                                                                                                                                                                                                                                                                                       seq_name==781,087 qeqdata/qeneseq_QeneseqqenNled=0A1_AAQ40513
                                                                                                                                         73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArqHisCysLeu
                                                                                            90 SorrysSerrysCysArglysSluMctGlyClsValGlalleScrSerCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "possible poly-A siqual"
                                                                                                                                                                                                                                                                                                                    190 AsnVallySCIyThrGluAspSerGlyThrThr 200
                                                                                                                                                                                                                                                                                                                              /product- p55 TNF-R
2143..2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phorbol myristate acetate; PMA; ss.
                                                                                                                                                                                                                                                                                                                                                                                  AAQ90513 standard; DNA; 2175 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9311.-0107268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94AU-0075742
                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                        p55 TNF-R gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-0CT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU9475742-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_siqual
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to different inducing agents, e.g. phorboi myristate accepte (MA), depending on cell type. The only region of the receptor whose structure affects the shedding response is the spacer region (see AAR75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the dys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimeras between human p55 TNF R and muniture epidenmal growth factor receptor (160F R) that are represented by AAR75007-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in AAR75017-9, AAR75025, AAR75033-5 and AAR75042.3. These protease
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents human p55 tumour necrosis factor (TNP-R) bNA. Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 INF-R can be shed in response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AAR75026-47). Of the spacer region, the most important residues are Asn 12., Val 17.5, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception or a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        These protease
                                                                                                                                                                                                   New protease capable of cleaving soluble tumour necrosis factor
                                                                                                                                                                                                                                             from cell-bound TNF- receptor, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 TRGGGGGACAGGAGAGAGAGATAGTGTGTGTGCCAAGGAAAATATATC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 CACCCTICAAAATAATTICGATTITGCTIGTACCAAGTGCCACAAAGGAAGCTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 GTGAGAGCGGCTCCTTCACCCTTCAGAAAACCACCTCAGACACTGCCTC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asps. (Valors Producting 12/8/17 | 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 rteuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 uLeuLeuValGlylleTyrProSerGlyValIleGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 HisProGlaAsaAsaSerIleCysCysThrLysCysHisLysGlyThrTy
Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitors can be used for enhancing TNF function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 94.787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAQ90513 from: 1 to: 2175
Batkin M, Brakebusch C, Variolomeev E,
                                                                                                                                                                                                                                                                               antagonising deleterious effects of INF.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1117.50
Ratio: 5.588
.milarity: 94.787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-525-998A-12 x AAQ90513
                                                                        WFI; 1995-194342/26.
                                                                                                                      P-PSDB; AAR75084
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                                                                                                                                                                                                                                             (TNF) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block
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90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106

us-09-525-998a-12.rng

Page 11

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SC 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant host cell; dihydrofolate reductase, selectable marker, DHFR: ras splice donor; dicistronic vector; gene expression; immunoadhesin; InFr-1gG; tumour necrosis factor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Improved process for the selection of pocombinant bost colls expressing high level of a desired product - uses eukaryotic host cells contg. a DNA construct comprising a selectable gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A dicistronic vector (AATISGA) Perrises a requisiony region derived from the eytomogalovitus immediate analygenes, a selectable dihyd. Clate calcutase give postfored within an intron having a 5 wild-type ras splice donor site, a downstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 AGCTGCTCCAAATGCCGAAAAJAAATGGGTCAGGTGGAGATGTGTTGTTG 605
                                                                                                                                                                                                   SThrValAspArgAspThrValCysClyCysArgLysAsnGlnTyrArgH 123
                                                                                                                                                                                                                                                                                                                              606 CACAGI GGACGGGACACCI GTG LGCCAGGAAGAAGCAG LACGGGC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 isiyrTrpgArdluAsnicaNhedinAysNteAsnOysSericuCysLea 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 AsnGlyThrValHisLeuSorCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 snCystystysterfeuGluCysThrLyst.cuCysteuProGInfleGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18: TVV IVO RELIVIOUS desentable for a second to the second of the second se
DHFR/intron (WTrasSD) - InFr - 1gG dicistronic vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AsnVallysGlyThrGluAspSerGlyThrThr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856 AATGITAAGGGGGGTGGGGGCCCAGGAA 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT15931;
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2005 ATTATRICAS: SAAAACCH FICCASTOCHT GAAR 100A5 ** , CIGCTIC 2454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 17 | UlcutteuVa | STYTTC| | YPP FOSE | TVA | HEGTY | TTTT | HELL | HEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1755 CACCCTCAAAAIAAITGGAFIITGCTGTACCAAGTGCCACAAAGGAACCIA 1804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeiCysLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AssStythiValEisLeuSerCyssloGluLyssloAssInValCysIb 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetGlyLeuSerIhuValProAspLeuLeuLeuProLeuValLeuLeuS; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .... AspSerValCysProGluGlyLysTyrlle 39
                                                 Sequence 6889 HP; 1729 A; 1826 C; 1681 G: 1654 1; 5 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2055 AATGGGACCGGCACTCTCCTGCCAGGAGAAACAGAACACGTGGCAC
                                                                                                                                                                                                                                                                                                                                                        Personal School of 1 141.787
                                                                                                                                                                                                                                                           lenqtii.
                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAli5931 from: 1 to: 6889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 AssNallys6lyThrGluAcpSerGlyThrFhr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV04431 standard: DNA: 6926 BP
                                                                                                                                                                                                                                                                                                       5,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-525-998A-12 x AAT15931
                                                                                                                                                                                                                                           Ouality: 1117.50
Rativ: 5.588
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                                                                                                                                                                                                          alignment_scores:
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pooris).
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Synthetic.

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening of compounds for ability to bind specific molecules - using a chimeric protein in which the specific molecule is fused to an immunoglobulin chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or ligand, e.g. in biomedical research and drug development. The method is especially intended for screening combinatorial libraries, but is also useful in screening bacterial/phage lysates, assays requiring specific binding partner interaction and obtaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the chimeric proteins, compounds can be rapidly screened for binding to an antigen, antibody, enuyme, encyme substrate, receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin regions recognising an epitope. A binding partner complex between the chimeric protein and compound(s) is formed, separated out and contacted with a (in)directly labelled secondary molecule which binds the 2nd domain, and the label detected. Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present vector, which is designated pcDNA3-IGGI-TNF-R and contains nucleic acid sequences encoding house immunoglobulin GI (IGGI) CH2. CH3 and binger regions and the human tumour necrosis factor receptor, was used in the development of a novel method of screening compounds for ability to bind a specific molecule. The method comprises contacting one or more compounds with a chimeric protein containing at least two domains, the 1st comprising a portion of the specific molecule, and the 2nd an immunoglobulin chain portion having one or more epitopes and/or
                                                                                                                                                      murine; mouse; immunoglobulin Gl; heavy chain; human; chimeric;
                                                                                                                                                                                         vector peDNA3-1961 NNF R; tumour nectosis factor receptor,
screening, combinatorial library; CM2; CM3; hinge region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6926 BP; 1638 A; 1816 C; 1765 G; 1707 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 94.787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aliqu seq 1/1 to: AAV04431 trom: 1 to: 6926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Pages 49-54; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHUG-) CHUGAI BIOPHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown SJ, Spinella DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding analogues of a compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US05821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0627151
27-APR-1998 (first entry)
                                                                              Vector pcDNA3-IqG1-TNF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aliqnment_block:
US-09-525-998A-12 x AAV04431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality, 1117.50
Ratio: 5.588
Wilarity: 94.787
                                                                                                                                                                                                                                                                                                        Chimeric - Mus sp.
Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-503233/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WU9737220-AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03 APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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INF: tumour necrosis factor; receptor; disease; autoimmunity; rheumatoid arthrilis; graff rejection; graff vs. host; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= p55 Tumour necrosis factor receptor
               1085 CACCCTCAAAATAATTGCTTGCTGTAGCAAGTGCCACAAAGGAACCTA 1134
                                                                                                                                                                                                                  1385 AATGGGACCGTGCACCHCTGCTGCCAGGAAACAGAACAGCGTGTGCAC 1434
                                                                                                                                                                                                                                                                                                                                  106 sThrValAspArgAspThrValCysGlyCysArqLysAsnGlnTyrArqH 123
                                                                                                                                                                                                                                                                   90 SerCysSerLysCysArgLysGluMetGlyGlnValGlulleSerSerCy 106
                                                                                                                                                                                                                                                                                                                                                                                                  123 isTyrTrpSerCluAsnLeuPheClnCysPheAssCysSerLeuCysLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 sudystystysserieudludysthrttysteudysteuprodiniledlu 189
                                                                                                                                 56 rLeuTyrAssAspCysProGlyProGlyGlnAspThrAspCysArqGluC 73
                                                                                                                                                                                                    73 ysGluSerClySerPheThrAlaSerGluAsnHisLeuArdHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDSz/qcqdata/qeneseq/qeneseqn/NA1993.DAT:AAQ50870
.....AspSerValCysProGlnGlyLysTyrlle
                                                                40 BisProCluAsnAsnScrilleCysCys On LysCysHistrysGlythriy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p55 Tumout necrosis factor receptor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 AsnValLysGlythrGluAspSerGlythrThr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ50870 standard; DNA; 2170 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256..1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      effector protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1993;
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Modification of the tumour necrosis factor receptor by mutation or deletion modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor. Molecules which interact with the TNF receptor or the effector proteins can be used to treat or prevent diseases associated with INF activity e.g. autoimmune diseases, rheumatoid arthritis; graft rejection, graft vs. lost disease or septic shock. They can also be used to treat overdoses of exogenous TNF.
                                                                                                                                                                                                                            Modulating activity of tumour nerrosis factor receptor - using peptide(s), antibodies, etc. which interact with critical remions of receptor or effector protein, for controlling auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 SThrValAsparjaspihrValCysClyCysArgLysAsnCluryTArgH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 CACCTICAAAATAATTGGATTTGCTGTACCAAGTGCAAAAGGAAGCTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 CACACLGGAPTCGGGAPACTGTGTGTGTTGTTGTAGGAAGAATTACTGGTT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 HisProGlaAsaAsaSerIleCysCysThrLysCysHisLysGlyThrTy 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 rLeuTyrAsnAspCysProGlyProGlyClnAspThrAspCysArgGluC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Met.GlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uLeuLeuValGlyIleTyrProSerClyValIleCly......29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ysCluSorGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2170 RP: 474 A: 657 C; 584 G; 455 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identily: 93.839
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                                                                                                                                                                                                                                                                                                                                                            Claim 2; Figure 1; 17pp; English
                                                 (YEDA ) YEDA RES & DEV CO LID.
9211, 0101769.
                                                                                                                                                                                                                                                                                                              discase, septic shock, etc.
                                                                                                    Brakebusch C, Wallach D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.543
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                                                                                                                                                   WP1; 1993-353057/45.
                                                                                                                                                                              P-PSDB; AAR42197.
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03-MAY-1992;
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/*tag- d
//abel-solutle_femain
/most mass bdl codons shorter or a few codons
| longer |
                                                          156 rCysHisAlaGlyPhePheLenArdCluAsnGluCysValSerCysSerA 173
                                                                                                                                                                                                                173 snCysLystycSérleuClaCycThrEyoLeuCysLeuProWhilleGlu 189
656 ATTATTONACTIMAAAACCTITTOMACTIOMATTOMACTIMICOMACTIMICOMA
                                                                                                                                                                                                                                                                                                                                                                  806 ACTOTARGAAAACCTGCAGTGCACAAAGTTGTGCCTACCTAGATTGAG 855
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/*tag= a
/.ote= "in frame terminat;on compon"
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/note= "IBP-1 derived sequence"
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//ote- "TBP I derived sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                190 AssVallysSlyThrSlyAspSerSlyThrThr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                             856 AAIGIIAAGAGCACIGAGGACTCA BOOGGCACA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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505. 633
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757..858
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The Tumour Necrosis Factor Binding Protein i is the soluble form of type I TMF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDMA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency.
                                                                                                                                                                                                                                                                                          Recombinant tumeur meerosis factor binding protein 1—prepd. by transfecting cukaryotic cells with vector contg. deoxyribonucleic acid encoding human type 1—INP receptor or soluble domain
                                                                                                                                                                                                      Wallach B, Nophal Y, Kempel O, Engelmann H, Brakebusch C;
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1(D), 30pp, English.
                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LID
                                                                                                   90EP-0124133.
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                                                                                                                                               8911.-0092697
 2145..2150
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 polyA_siqual
                                                                                                                                12-JUL-1990;
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                                                                                                                                             13-DEC-1989;
                                                                       26-JUN-1991
                                          EP433900-A
                                                                                                                                                                                                                       Aderka D;
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Ratio: 5.565 Gaps: 1 Percent Similarity: 94.313 Percent identity: 94.313 Length: Ouality: 1107.50 aliqnment_scores: aliqnment_block:

Sequence 2176 BP, 475 A, 644 C, 602 G, 455 T, 0 other;

See also AAQ12212-15.

 $0.9 - 5.25 - 998A - 12 \times AAQ12215$

Align seg 1/1 to: AAQ12215 from: 1 to: 2176

.AspSerValCysProGlnGlyLysTyrIle 39 30

40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 56

356 TAGGGGAGAGAGAGAGAGATAGTGTGTGTGCCCAAGGAAATATATC 405

56 rl.eufyrAsnAspCysProGlyProGlyClnAspThrAspCysArgGluC 73

73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89

90 SercyssertyscysArgtysGlaMetGlyGlnValGLulleSerserCy 106

190 AsaVallysClyThrGluAspSerClyThrThr 200

